

CaI	PVAALKEKS-HTEKVEQALND-PKKHVIVAMAPSVRTAMGELFKMGYGKD	247
CpI	PVAALSEKS-HMDRVKNALNA-PEKHVIVAMAPSVRASIGELFNMGFGVD	248
Dd	PENATYEAQSWVPEVEKKLKD-GAVKCIAMPAPAVRYALGDAFGMPVGSV	98
CrHydA2	ATDAVPHWKLAEEEDDKPKDG-GKVKVIAQVAPAVRVAAEESFGLAPGAV	113
CrHydA1	AEAPLSHVQQAFAEAAKPKDDPTKHKVCVQVAPAVRVAAETLGLAPGAT	110
CaI	VTGKLYTAMMTEGDKVMDINFGEMTEGEEAEEGGRK-----NN	289
CpI	VTGKLYTALRQLGFDKEDINFGEMTEGEEAEEGGRKE-----NN	290
Dd	TTGKMLAALQKLGFAHCWDTEFTADVTTIWEPEGSEEFVERITK-----KSD	142
CrHydA2	SPGKRLATGTTRAETGQFETLFAELTETMEEGSELEHREKEHLEAHPHSD	163
CrHydA1	TPKQLAEGLRRLGFDDEVFDTLFGADLTIMEEGSELEHRETEHLEAHPHSD	160
CaI	GPEPMTFTSCCPAWVRLKQNYHPELFDNLSSAKSPQIFGTASKKTYPSIS	339
CpI	GPEPMTFTSCCPGWVRLKQNYHPELFDNLSSAKSPQIFGTASKKTYPSIS	340
Dd	MPLPQFTSCCPGWQKYAETYPPELPHFSTCKSPIGMNGALAKTYGAERM	192
CrHydA2	EPLPMTFTSCCPGWVAMMEKSYPELEFPVSSCKSPQMMMGAMVKTYLSEKQ	213
CrHydA1	EPLPMTFTSCCPGWIAMLEKSYPDLLIPYVSSCKSPQMLAAMVKSYLAEEK	210
CaI	GLAPEDVYTVTIMPNCNDKKYEADIPFMETNS---LRDIDASELTTRRELAKM	386
CpI	GLDPKNVFTVTVMPCTSKKFEADRPQMEKDG---LRDIDAVITTRRELAKM	387
Dd	KYDPKQVYTVSIMPICIAKKYEGLRPELKSSG---MRDIDATETTRRELAYM	239
CrHydA2	GLPAKDITVMVSVMPICVRKQGEADREWFVCVSE-PGVRDVDHVITTAELGNI	262
CrHydA1	GLAPKDMVMVSLMPICTRKQSEADRDWFCVDADPTLRQVDHVITTVELGNI	260
CaI	TKDAKIKFADLEDGEVDPAMGTYSAGAGATFCATGGVMEAAALRSAKDEAEN	436
CpI	TKDAKIPFAKLEDSEADPAMGEYSAGAGATFCATGGVMEAAALRSAKDEAEN	437
Dd	IKKAGIDFAKLPDGKRDLSLMGESAGGATFCGVTGGVMEAAALRFAYEAVTG	289
CrHydA2	EKERGINLPELPDSDDWDQPLGLGSGAGVLEFGTTGGVMEAAALRTAYEITVK	312
CrHydA1	EKERGINLAELPEGEWDNPMGVGSGAGVLEFGTTGGVMEAAALRTAYEITVK	310
CaI	KELENVDYTEVRGFKGIKEAEVEETA-----	461
CpI	AELEDTEYKQVRGLNGIKEAEVEETN-----	462
Dd	KKPDSWDFKAVRGLEDGIKEATVNVG-----	314
CrHydA2	EPLPRENLSEVRGLEDGIKEASVTLPVPAPGSKFAELVAERLAHKVEEAAAA	362
CrHydA1	TPLPRELSLSEVRGMDGIKETNTMTVPAPGSKFEEELKHRAAARAEAAAHG	360
CaI	-----GNKLNVAVINGASNRFEFMKKS	482
CpI	-----NNKYNVAVINGASNLFKFMKS	483
Dd	-----GTDVKVAVVHGAKRFKQVCDD	335
CrHydA2	EAAAAVEGAVKPPPIAYDGGQGFSTDDGKGGLKLRVAVANGELGNACKKLIK	412
CrHydA1	TPG-----PLAWDGGAGFTSEDGRGGITLRVAVANGELGNACKKLITK	401
CaI	GKMNEKQYHFEVEMACPGGCINGGGQPHVNALDRENVDIRKCLRASVLYNQ	532
CpI	GMINNEKQYHFEVEMACHGGCVNGGGQPHVNPKDLEKVDIKKVRASVLYNQ	533
Dd	VKAGKSPYHFEVEMACPGGCVCVGGGQPVMPGVLEA-----	370
CrHydA2	MVSGEAKYDVEVEIMACPAAGCVGGGGQPRSTDQKITQK-----RQAALYDL	457
CrHydA1	MQAGEAKYDVEVEIMACPAAGCVGGGGQPRSTDKAITQK-----RQAALYNL	446

Fig. 1A

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Fig. 1B

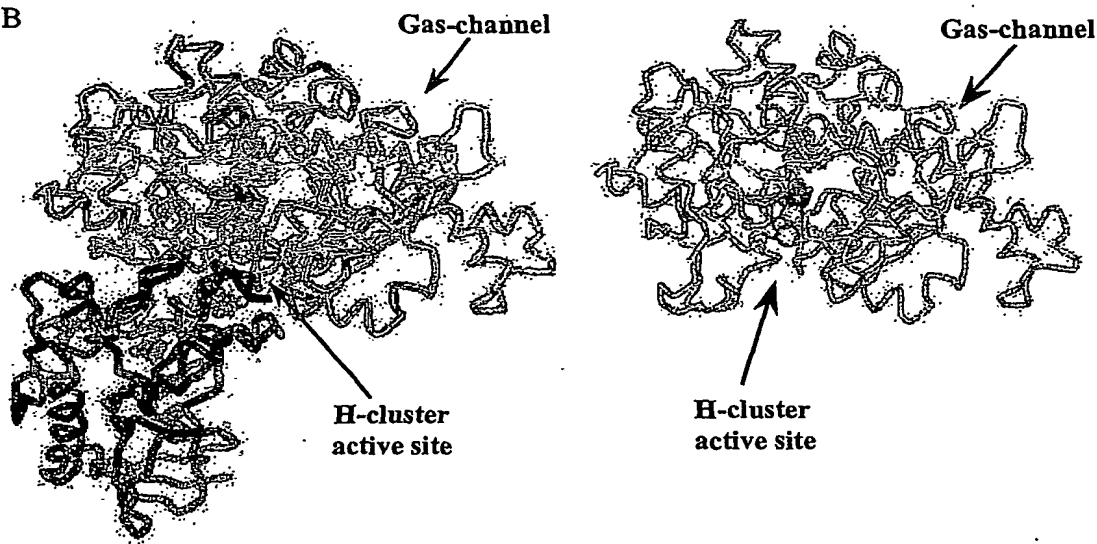


Fig. 2

Cr HydA1	AAPAAEAPLSHVQQALAEALAKPKDDPTRKHVCVQVAPAVRVAIAETLGLAPGATTPKQLA	60
CpI	CIIACPVAALSEKSHMDRVKNALNAPEKHVIVAMAPSVRASIGELFNMFGVDVTGKIY	59
Cr HydA1	EGLRRLGFDDEVFDLFGADLTIMEESELHRRITTEDEPLPMFTSCCPGWIAMLEKSYDDL	120
CpI	TALRQLGFDKIFDINFGADMTIMEESELVORLENNGPFPMTSCCPGWVRQAENYYPEL	119
Cr HydA1	IPYVSSCKSPQMMLAAMVKSYLEKKGIAPKDMVMVSIMPCTRKQSEADRDWFCVDADPT	180
CpI	LNNLSSAKSPQQIFGTASKTYYPISGLDPKNVFTVTVMPCTSKKFEADRPQMEKDG---	176
Cr HydA1	LRQLDHVITTVELGNIFKERGINLAELPEGEWDNPMGVGSGAGVLFGTGGVMEAAALRIA	240
CpI	LRDIDAVITTRELAKMIKDAKIPFAKLEDSEADPAMGEYSGAGAIFGATGGVMEAAALRSA	236
Cr HydA1	YVETGTGPLPRLSLSEVRGMDGIKETNITMVPATLRVAVANGLGNAKKLITKMQAGEAKY	300
CpI	KDEAENAELEDIEYKQVRGLNGIKEAEVEINNNKYNVAVANGASNLFKFMKSGMINEKQY	296
Cr HydA1	DEVDIMACPAGCVGGGGQPRSTDKAITQKRQAALYNLDEKSTLRRSHENPSIRELYDTYL	360
CpI	HEDEVMACHGGCVNGGGQPHVNPDKIKVRASVLYNQDEHLSKRKSHENTALVKMYQNYF	356
Cr HydA1	GEPLGHKAHELLHTHYVAGGVEEKDEKK	388
CpI	GKPGEGRAHEILHFKYKK-----	374

Fig. 3

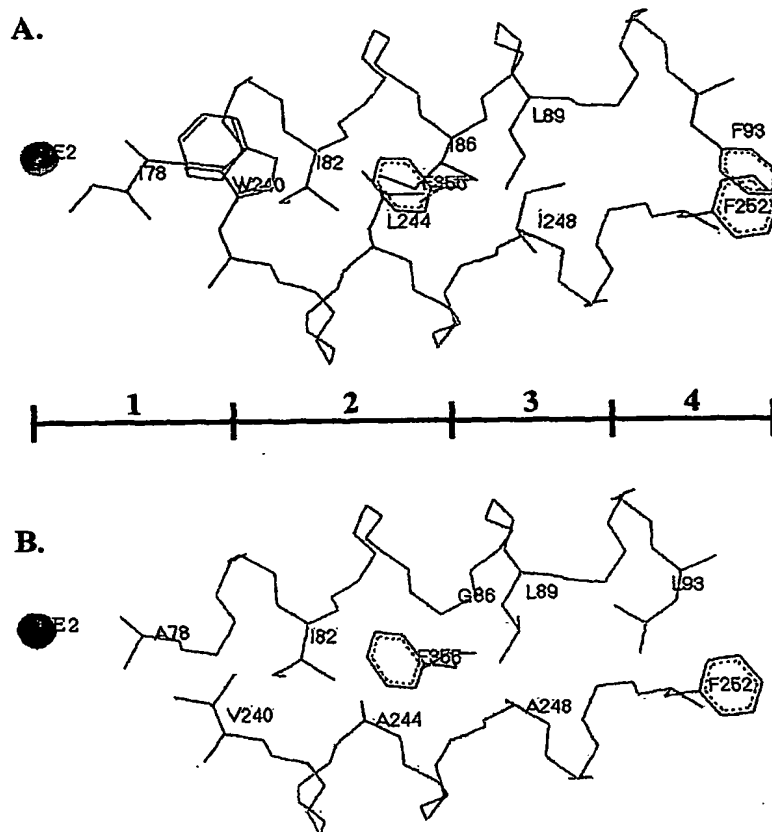


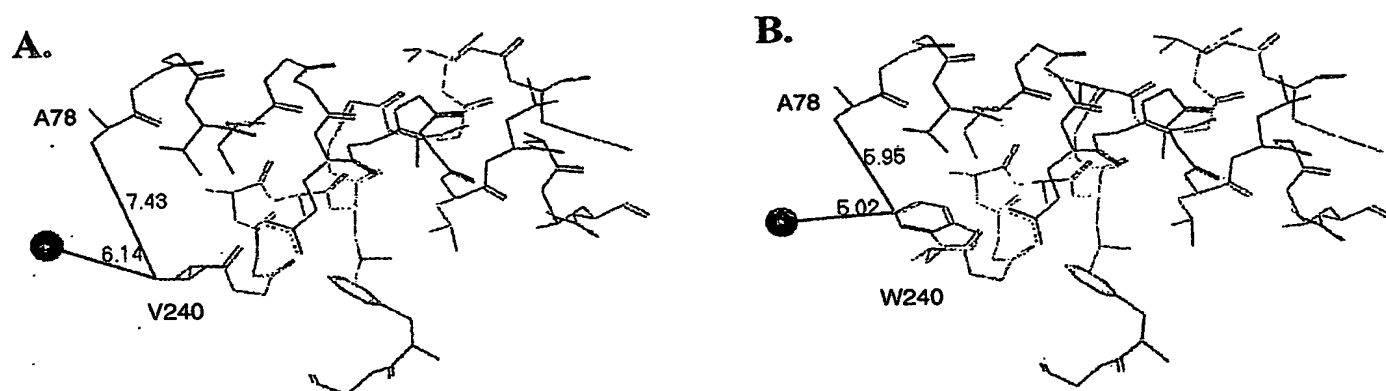
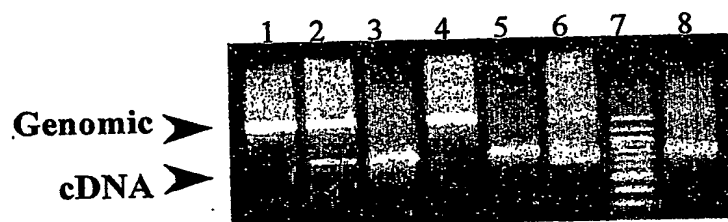
Fig. 4**Fig. 5**

Fig. 6

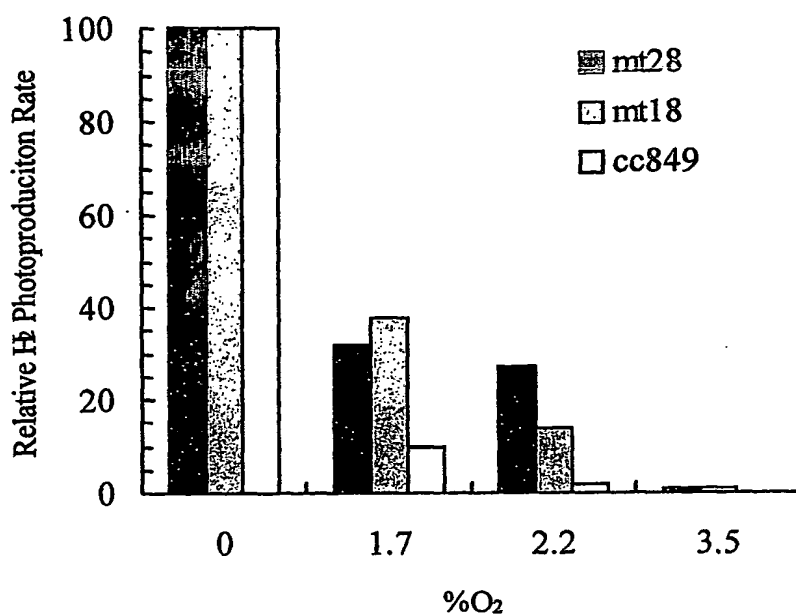
H₂ Electrode Assay

Fig. 7

MV Assay

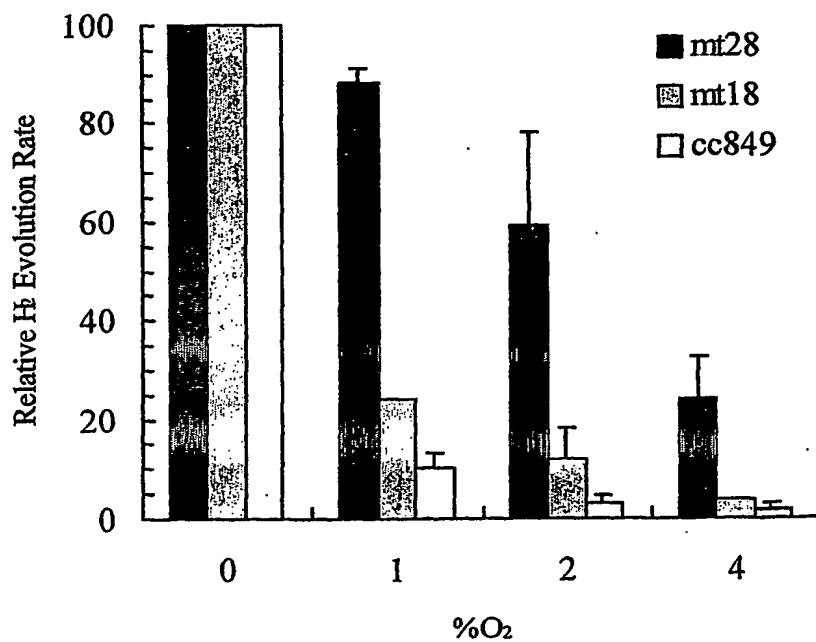
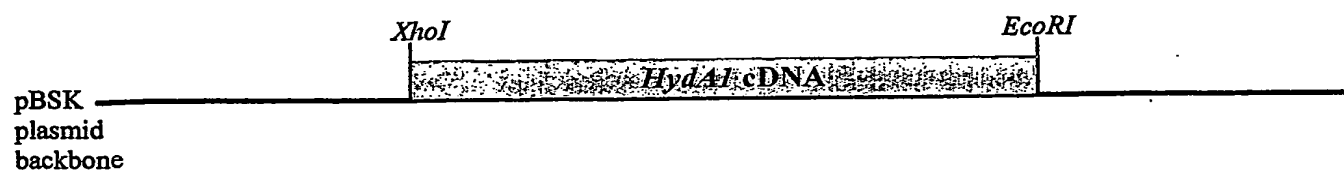
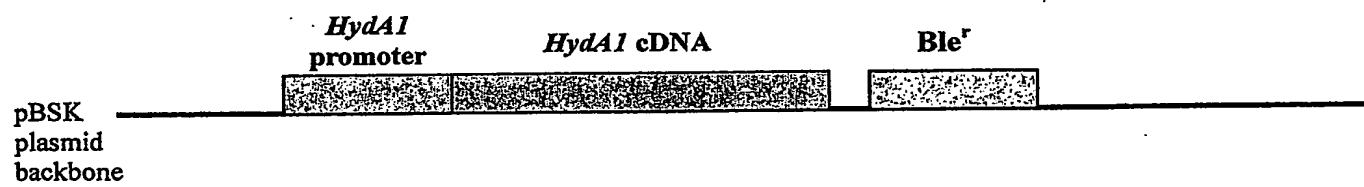


Fig. 8**Fig. 9**

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